

Shown is the 3'UTR of the human IL1B sequence from accession number M15330.

* Represents the stop codon.

*AGAGAGCTGTACCCAGAGAGTCCTGTGCTGAATGTGGACTCAATCCCTAG
GGCTGGCAGAAAAGGGAACAGAAAGGTTTTTGAGTACGGCTATAGCCTGGAC
TTTCCTGTTGTCTACACCAATGCCCCAACTGCCCTGCCCTTAGGGTAGTGCTAA
GAGGATCTCCTGTCCATCAGCCAGGACAGTCAGCTCTCTCCTTTCAGGGCC
AATCCCAGCCCTTTTGTGAGCCAGGCCCTCTCTCACCTCTCCTACTCACT
TAAAGCCCGCTGACAGAAACCAACGCCACATTTGGTTCTAAGAAACCCCTC
TGTCATTGGCTCCACATTCTGATGAGCAACCGCTTCCCT**ATTTATTATT**
TATTTGTTTGTGTTTATTCAATTGGTCTAATTTATTCAAAGGGGCAAG
AAGTAGCAGTGTCTGTAAAAGAGCCCTAGTTTTTAATAGCTATGGAATCAAT
TCAATTTGGACTGGTGTGCTCTCTTTAAATCAAGTCCTTTAAATTAAGACTG
AAAATATATAAGCTCAGATTATTTAAATGGGAATATTTATATAAATGAGCAAA
TATCATACTGTTCAATGGTCTCTGAAATAAACTTCTCTGAAG

FIGURE 1

ATGGCTTCCCT**ATTTATTTATTTATTT**TTTGTTCACCT
|||||
GGATACCGAAGGA**TAAATAAATAAATAA**CAACAGGTT

FIGURE 2

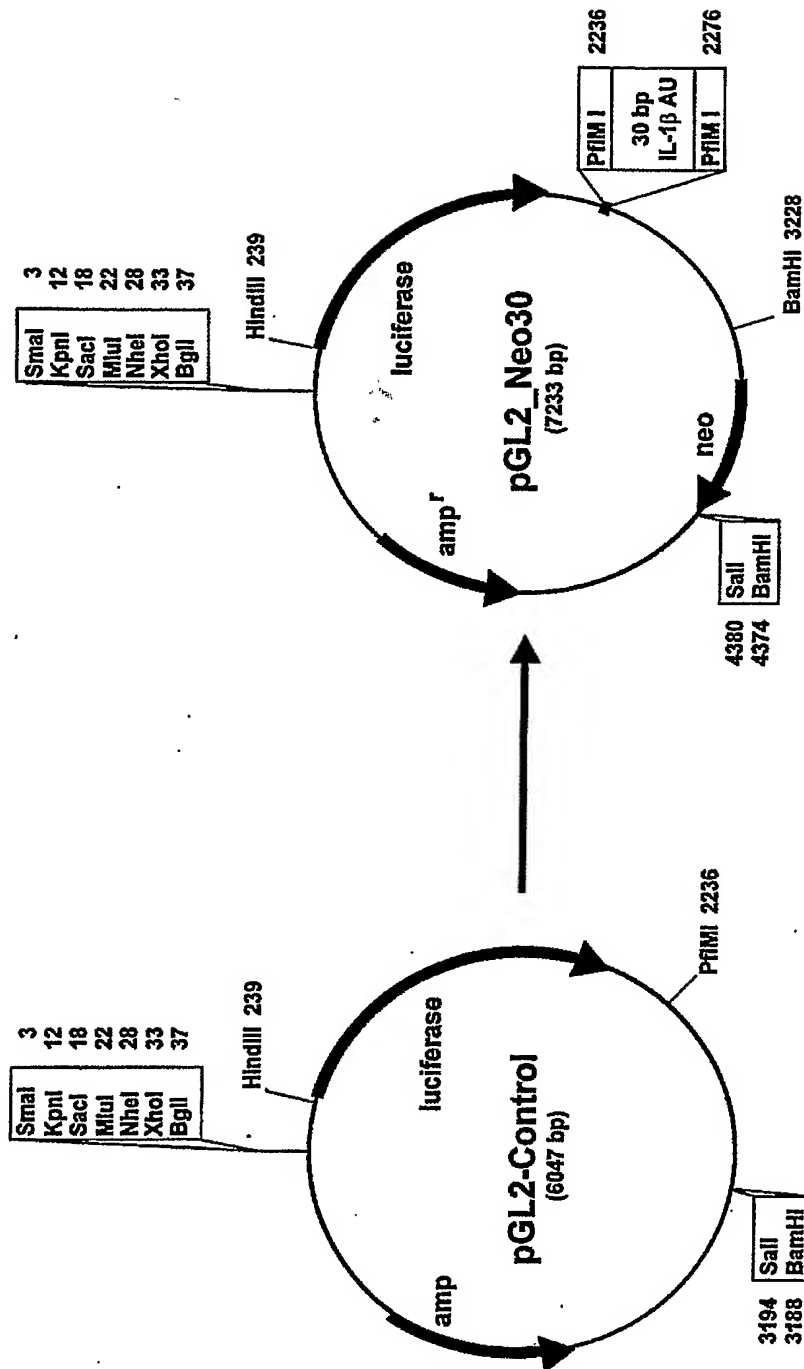


FIGURE 3A

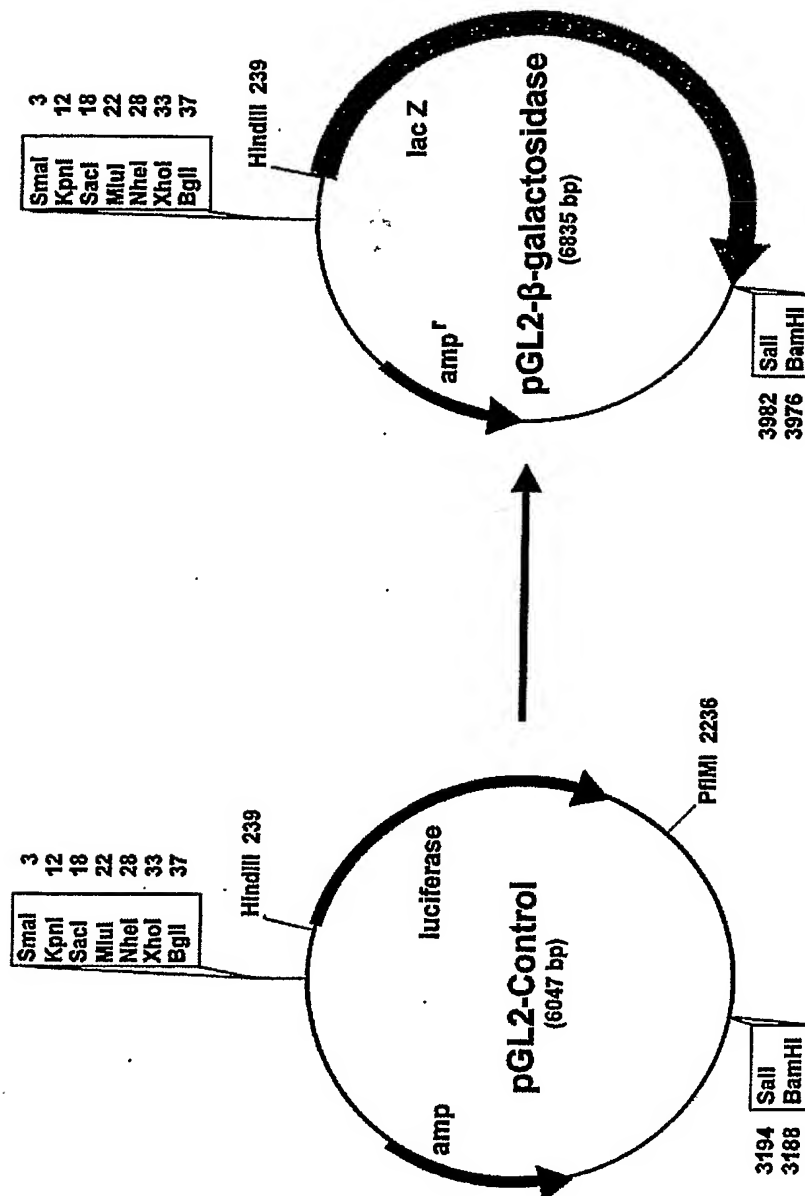


FIGURE 3 B

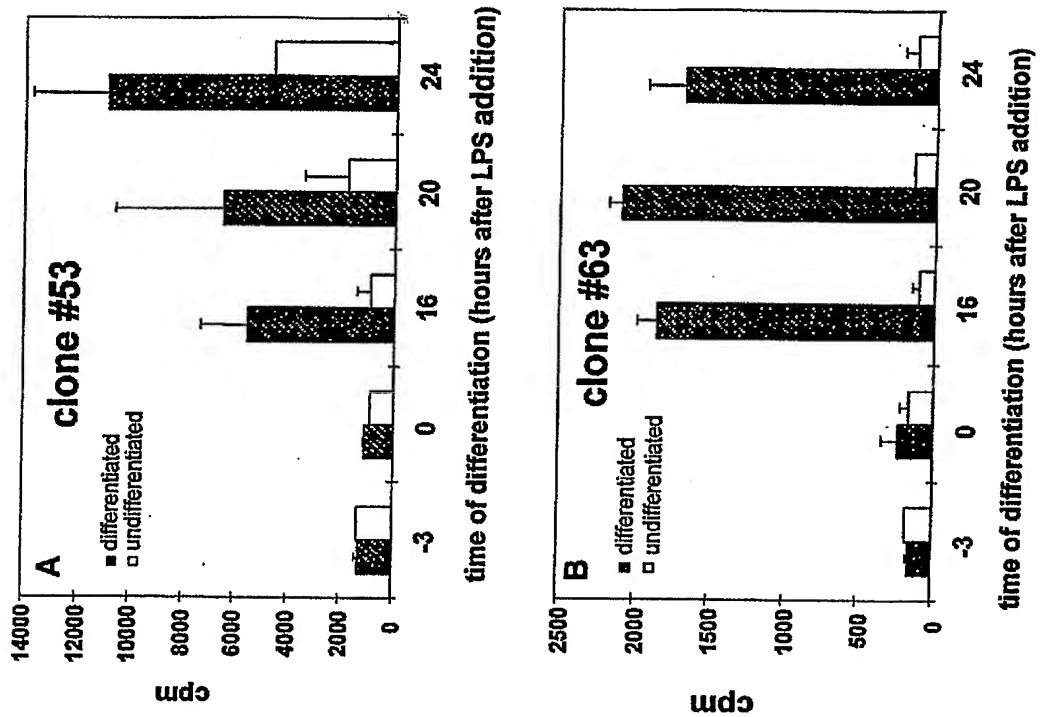


FIGURE 4

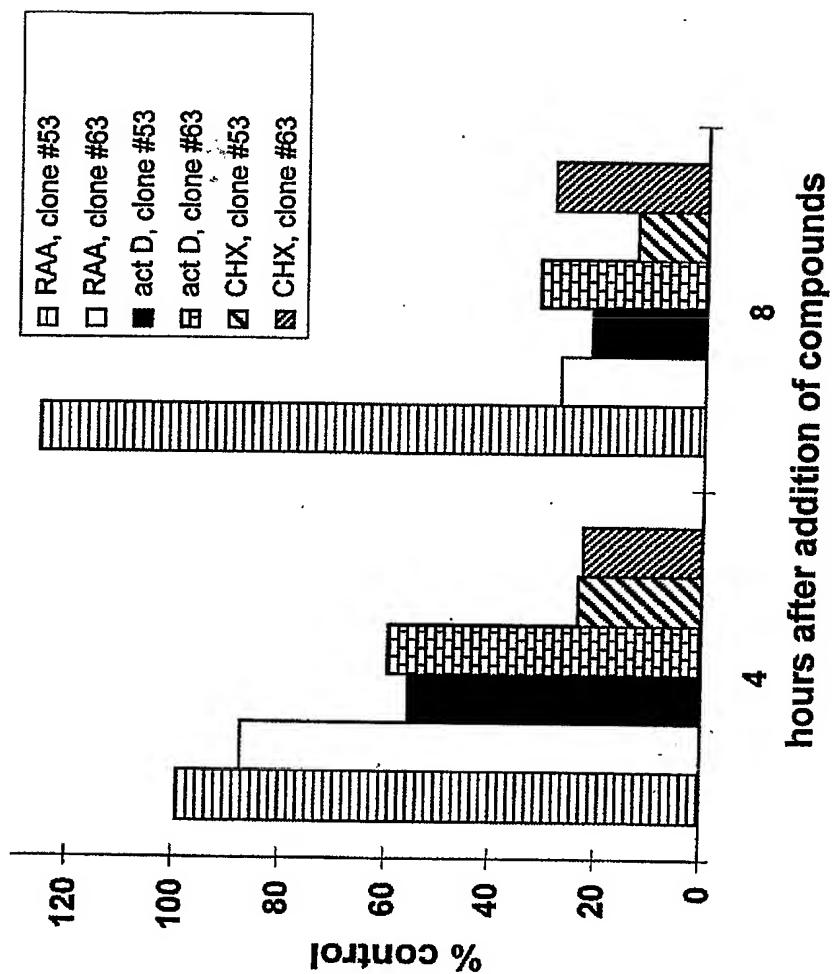


FIGURE 5

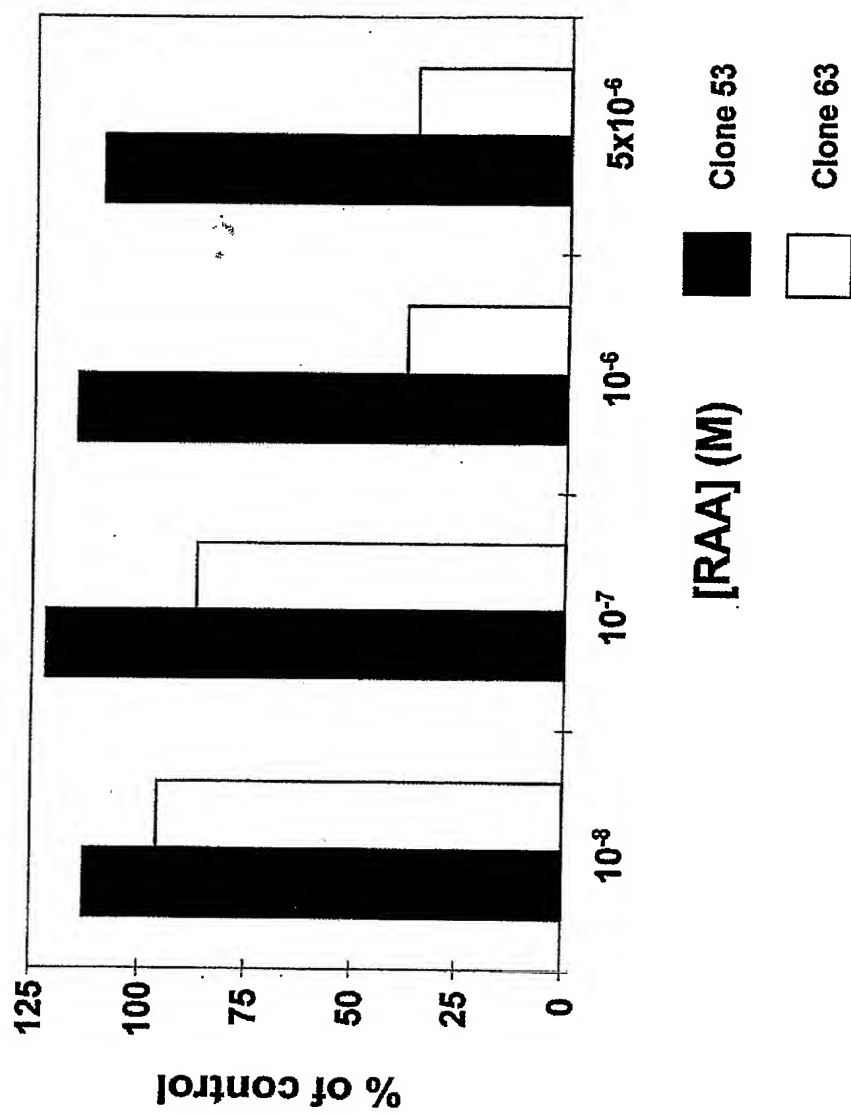


FIGURE 6

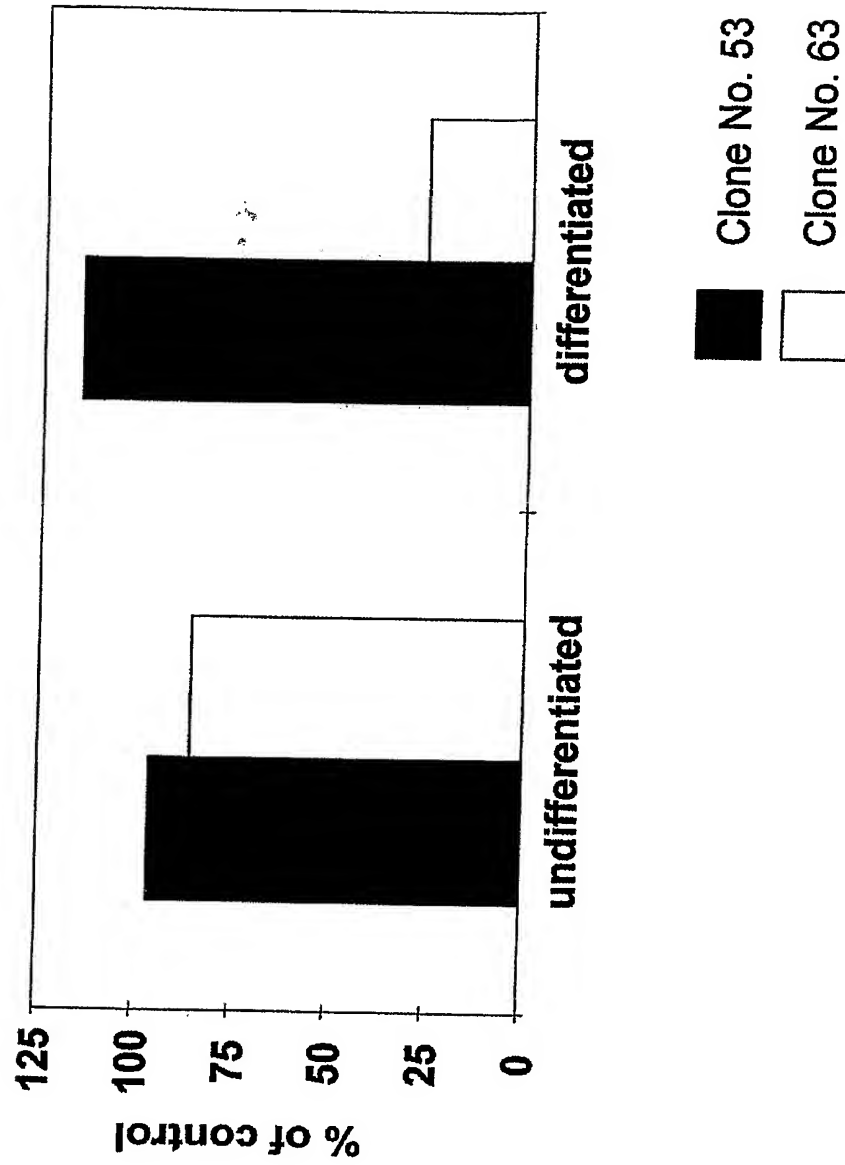


FIGURE 7

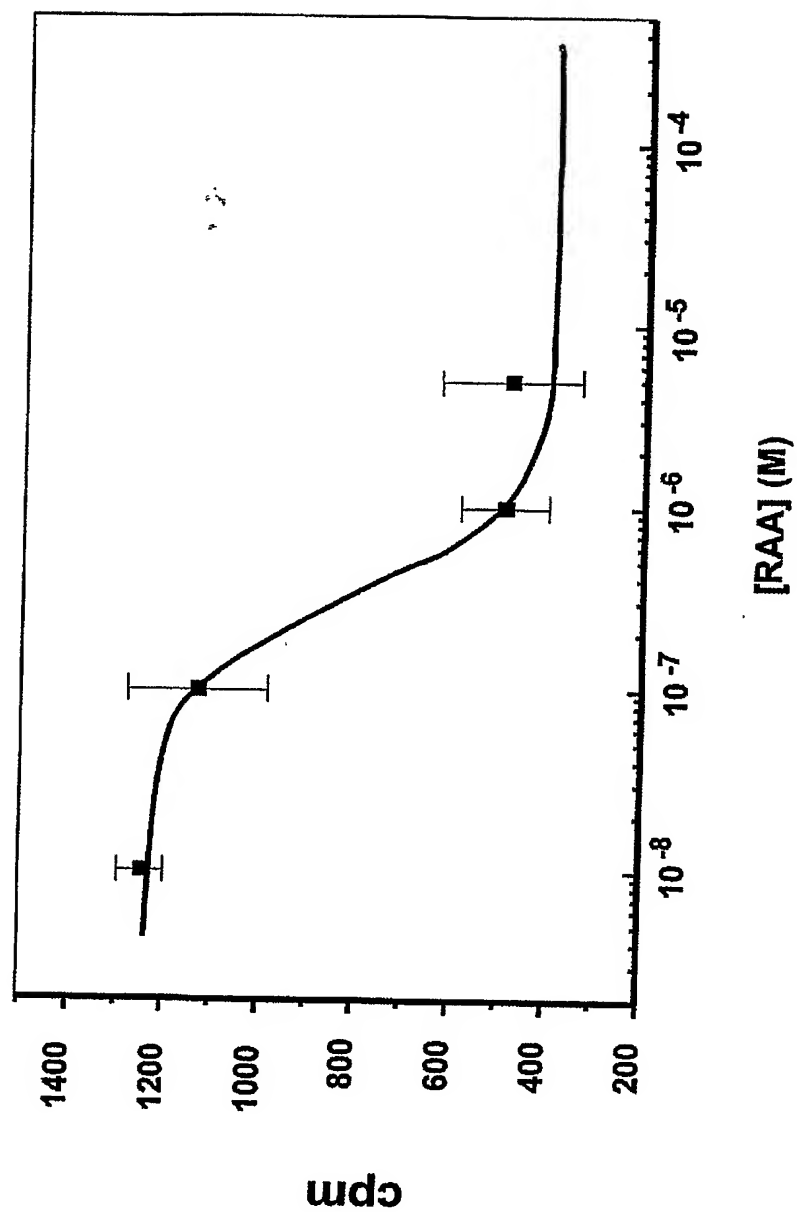
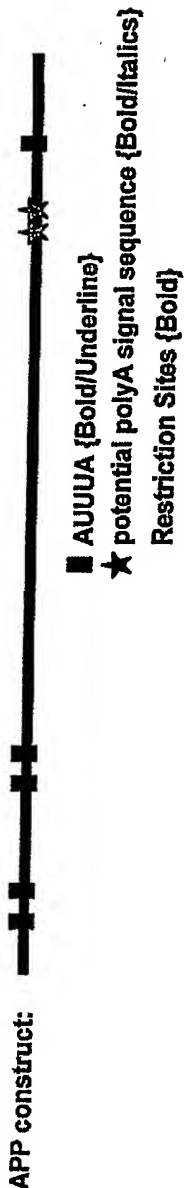


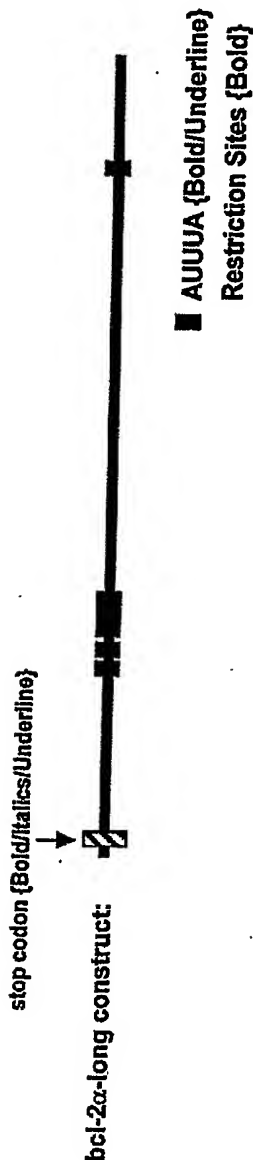
FIGURE 8

APP construct: 

■ AUUUA {Bold/Underline}
 ★ potential polyA signal sequence {Bold/Italics}
 Restriction Sites {Bold}

	NotI	
1	GGGCGCGCA CAGCAGCCTC TGAAGTTGGA CAGCAAAACC ATTGCTTCAC TACCCATCGG TGTCCATTAA TAGAATAATG TGGGAAGAAA CAAACCCGTT	
101	TTATGATTAA CTGATTATCG CCTTTTGACA GGTGTGCTGT AACACAAGTA GATGCTGAA CTTCGAATTAA TCCACACATC AGPRAATGAT TCTATCTCTC	
201	TTTACATTTT GGTCTCTATA CTACATTATT AATGGGTTTT GTGTACTGTA AAGAAATTAG CTGTATCAAA CTAGTCCATG AATAGATTCT CTCCTGATTAA	
301	TTTATCACAT AGCCCCCTAG CCAGTTGTAT ATTATTCCTG TGGTTGTGA CCCAATTAAG TCCCTACTTA CATATGCTTT AGAATTCGAT GGGGGATGCT	
401	TCATGTGAAC GTGGGAGTTC AGTGTCTCT CTGCCCCTAAG TATTCCTTTC CTGATCACTA TGCATTTTAA AGTTAAACAT TTTTAAAGTAT TTCAGATGCT	
501	TTAGAGAGAT TTTTTTTTCC ATGACTGCAT TTACTGTAC AGATTGCTGC TTCTGCTATA TTGTGTATAT AGGAATAAG AGGATACACA CGTTTGTTC	
601	TTGCTGCCCTG TTTTATGTGC ACACATTAGG CATTGAGACT TCAGCTTTT CTTTTTTTGT CCAGTATCT TTGGTCTTT GATAAAGAAA AGAATCCCTG	
701	TTCAATTGTAA GCACTTTAC GGGCGGGTG GGGAGGGTG CTCGCTGGT CTTCATTAC CAAGAATCT CCAAAACAAT TTTCTGCAGG ATGATTGTAC	
801	AGAATCATFG CTTATGACAT GATCGCTTTC TACACTGTAT TACATAAATA AATTAATAA AATAACCCG GSCAAGACTT TTCTTTGAAG GATGACTACA	
901	GACATTAAAT AATCGAAGTA ATTTTGGCTG GGGAGAGAG GCAGATTCAA TTTTCTTTAA CCAGTCTGAA GTTTCATTAA TGTATACAAA GAAGATGAAA	
1001	ATGGAAGTGG CAATATAAGG GGATGAGGA GGCATGCCCTG GACAACCCCT TCTTTTAAAG TGTGTCTTCA ATTGTATYAA AATGGTCTTT TCATGTAGCG	
1101	GCGGC	NotI

FIGURE 9 Length: 1105 bp



	NotI
1	GGGGGGCTG <u>AGTCAACAT</u> GCCTGCCCCA ACAAATATG CAAAGGTTT ACTAAAGCAG TAGAAATAT ATGCATTGTC AGTGATGTAC CATGAACAA
101	AGCTGAGGC TGTTHAGAA AAAATACAC ACATATTAAC ATCACACACA CAGACAGACA CACACACACA CAGCTTTCAG GORAAAGTC
201	GAATCAGCTA <u>TTTACTGCCA</u> AAGGGAATA <u>TCATTTATTT</u> TTTACATAT TAAGAAAAA AGATTATTT <u>ATTTAAGACA</u> GTCCATCAAA AACTCCTGTC
301	TTTGGAAATC CGACCACTAA TTGCCAAGCA CGCTTCGTG TGGCTCCACC TGGATCTCT GTGCTGTAA ACATAGATT GCTTTCCANG TTGTTGCCG
401	GATCACCATC TGAAGAGCAG ACGGATGGAA AAAGGACCTG ATCATTTGGG AAGCTGGCT TCTGGCTGCT GGAGGTGGG GAGAAGGTGT TCHTTACATT
501	GCAATTTCTT GCCCTGGGG CTGTGATATT AACAGAGGGA GGGTTCCTGT GGGGGGAAGT CCATGCCCTCC CTGGCTGTA GAAGAGACTC TTTGCATATG
601	ACTCACATGA TGCATACCTG GTGGGAGGAA AAGAGTTGGG AACTTCAGAT GGACCTASTA CCCACTGAGA TTTCACGCCG GAAGGACAGC GATGGGAAA
701	ATGCCCTTAA ATCATAGAAA AGTATTTTT TAAGCTACCA ATTGTGCCG GAAAGCAAT TTAGCAATTT <u>ATACAATATC</u> ATCCAGTACC TTAAGCCCTG
801	ATTGTGTATA TTCATATATT TTGGATACGC ACCCCCCAAC TCCAAATCT GGCCTGTCT GACTAAGAAA CAGATCTCTC TGGAACTTGA GGAAGTGGG
901	CCGC
	NotI

Length: 904 bp

FIGURE 10

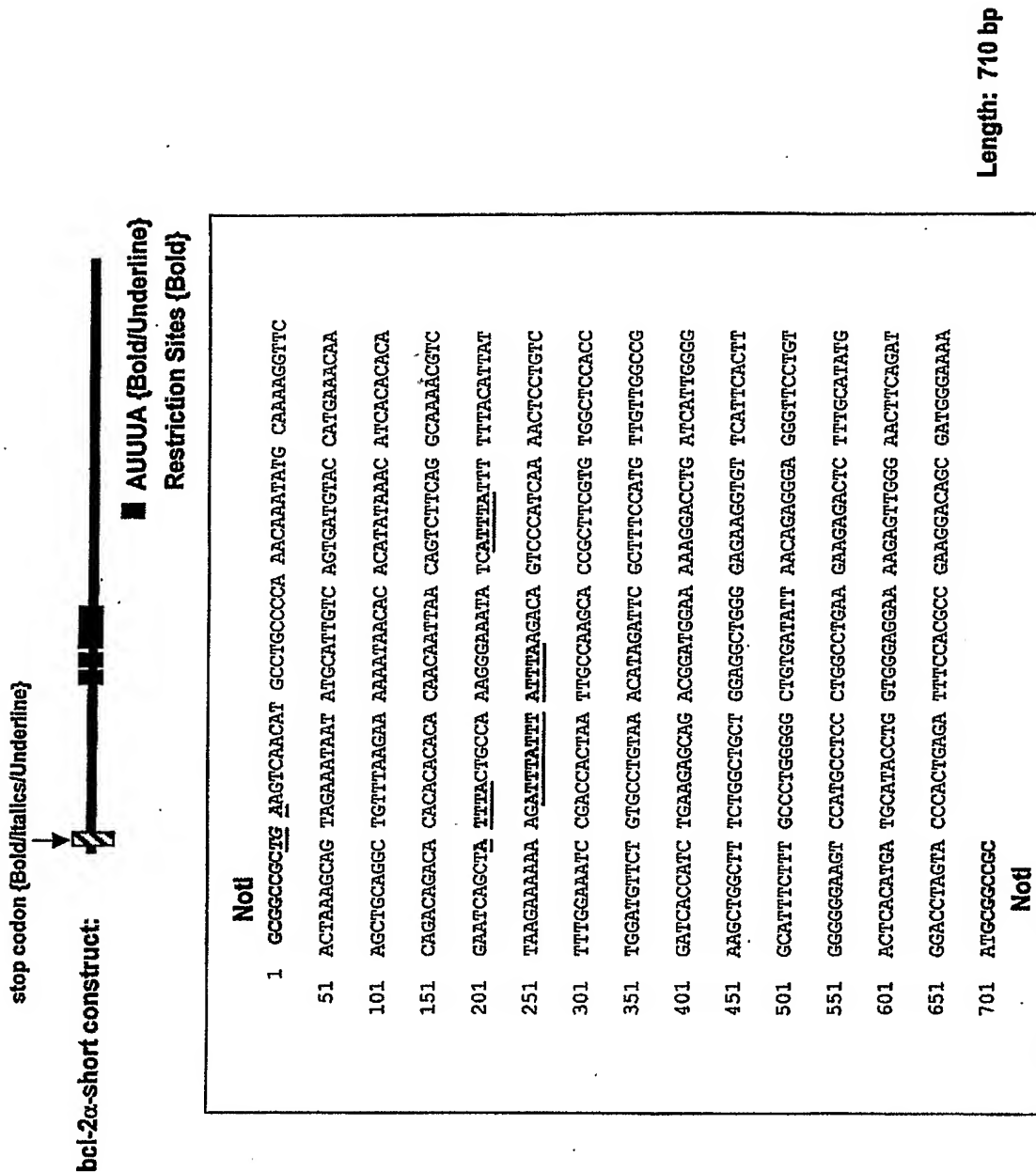


FIGURE 11

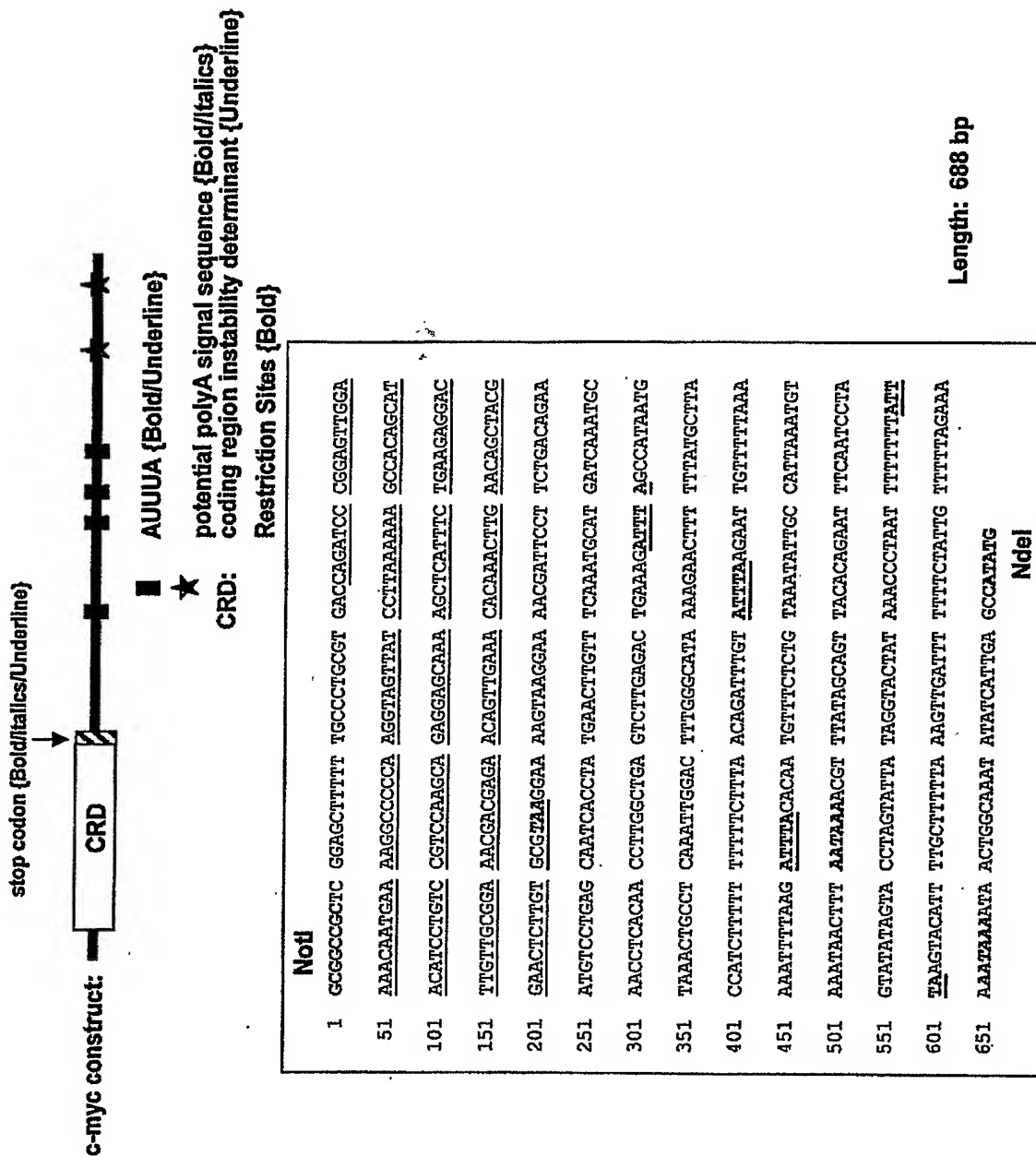


FIGURE 12

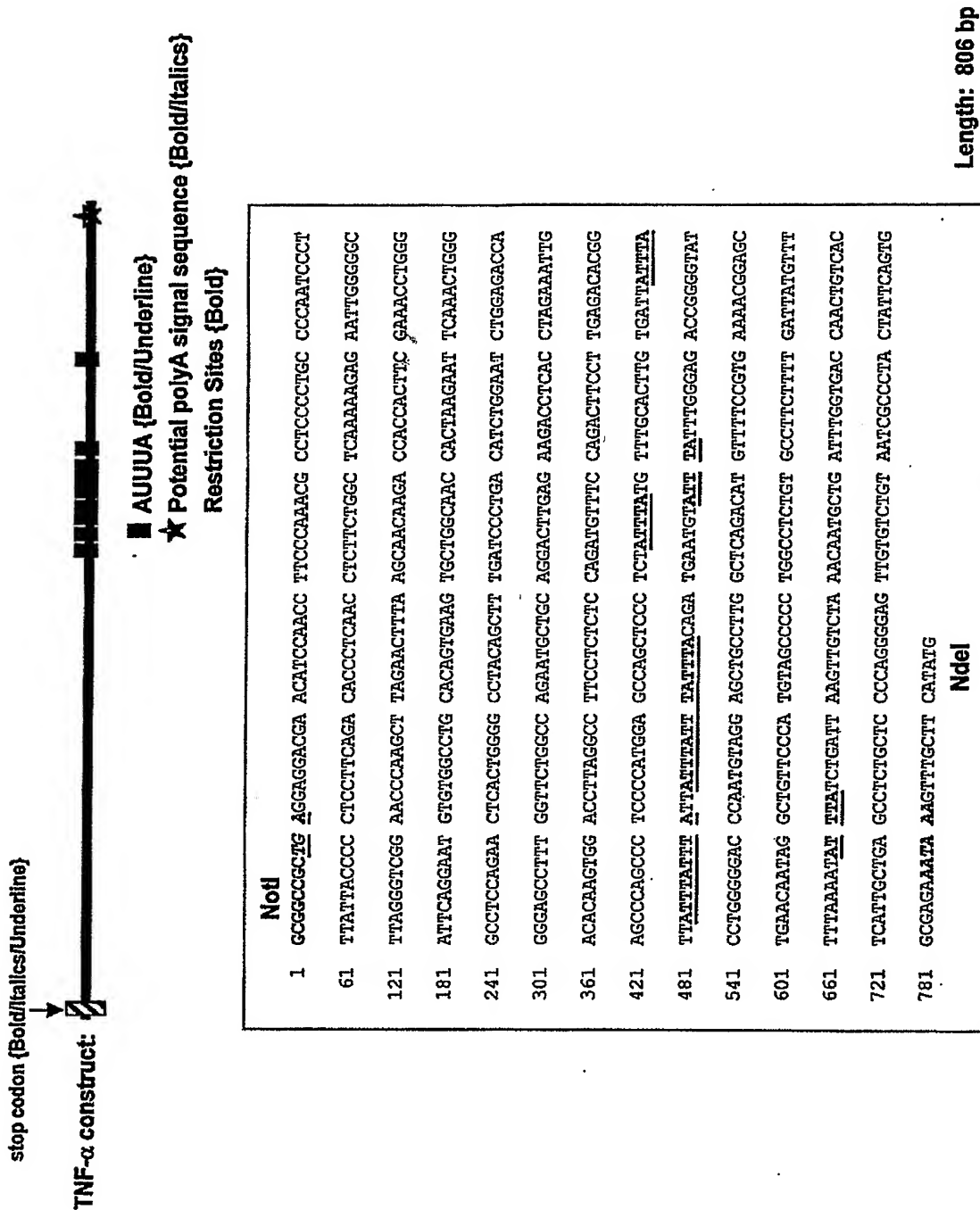
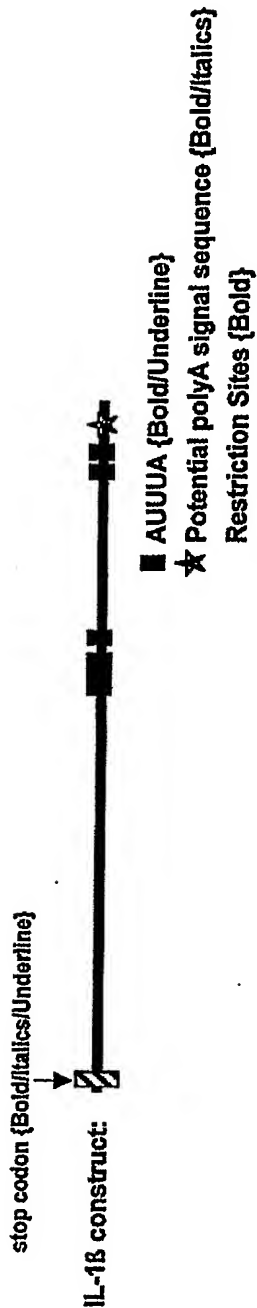


FIGURE 13



VEGF construct: 

- AUUUA {Bold/Underline}
- ★ Potential polyA signal sequence {Bold/Italics}
- Restriction Sites {Bold}

	NotI
1	GGGCGGCGCAT TCGTGTGCTT TGGGGATTCC CTCACGCGCA TCTCGCCCCC AGGGGCACTG CTGGGAGAT TCAGGAGCCT GGGCGGCGCTT
101	CGCTTACTCT CACCTGCTTC TGAGTTGCCC AGGAGGCCAC TGGCAGATGT CCGGGCGGAG AGAAGAGACA CAATGTTGGA AGAAGCAGCC CATGACAGCT
201	CCCCCTCCTG GGAATCGGCC TCATCCTCTT CCTGCTCCCT TTCTGCGGCT GCAGCCTAAA AGGACCTATG TCCTCAGACC ATTGAAACCA CTAGTTCTGT
301	CCCCCGAGGA GACCTGGTGG TGTGTGTGTG AGTGGTTGAC CTTCCTCCAT CCGCTGGTCC TTCCCTTCCC TTCCCGAGGC ACAGAGAGAC AGGSCAGGAT
401	CCACGTGCCC ATTGTGGAGG CAGAGAAAG AGAAGTCTT TTATATACGG TACTTATTTA ATATCCCTTT TTAATTAGAA ATTAATAACAG TTAATTTAAT
501	TAAAGAGTAG GGTGTTTTTT CAGTATCTT GGTAAATATT TAATTTCAAC TATTATGAG ATGTATCTTT TGCTCTCTCT TGCTCTCTTA TTGTACCGG
601	TTTTTGTATA TAAATTCAT GTTCCCATC TCCTCTCCC TGATCGGTGA CAGTCACTAG CTTATCTTGA ACAGATATTT AATTGTCCTA ACATCAGCT
701	CTGCCCTCCC CGATCCCCCTG GCTCCCCAGC ACACATTCCT TTGAATAAAG GTTCAATPAT ACATCTACAT ACATATATA TATATTGGC AACTTGTATT
801	TGTGTGTATA TATATATATA TATGTTTATG TATATATCTG ATTCTGATTA AATAGACATT GCTATCTCT TTTTATATATG TAAATACAAA ACAGAAAAA
901	ATAGAGAAAT CTACATACTA AATCTCTCTC CTTTTTAAAT TTTAATATTT GTTATCAATTT ATTATTTGCT GCTACTCTTT ATCCCTAATA ATTGTGGGA
1001	AAAGATATTA ACATCAGCTC TTGTGCTCTA GTGCACTTTT TCGAGATATT CCGTAGTACA TATTATTTTT TAAACAACGA CAAGAAAAA CAGAACATAT
1101	NdeI
1101	G

Length: 1101 bp

FIGURE 15

VEGF 3'UTR hypoxia domain construct: 

■ AUUUA {Bold/Underline}
Restriction Sites {Bold}

	NotI
1	GCGGCCGCAT TCCTGTAGAC ACACCCACCC ACATACATAC <u>ATTTATATATAT</u>
51	ATATATATTA TATATATATA AAAATAAATA TCTCTATTTT ATATATATAA
101	AATATATATA TTCTTTTTTT AAATTAACAG TGCTAATGTT ATTGGTGTCT
151	TCACTGGATG AACATATG
	NdeI

Length: 168 bp

FIGURE 16

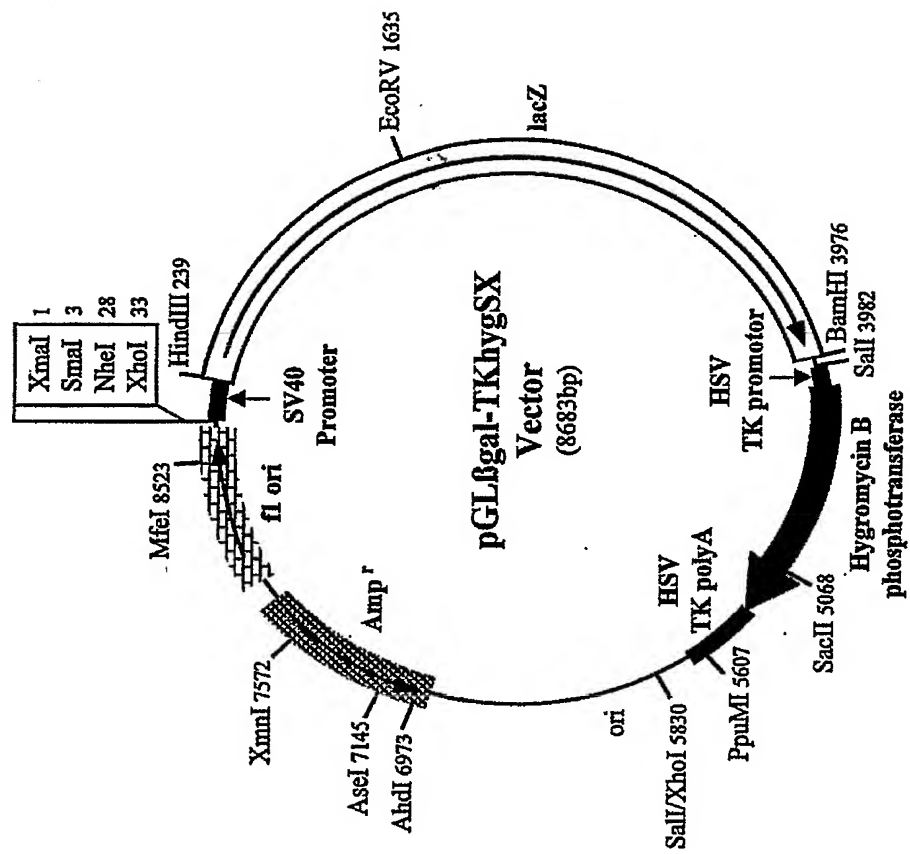


FIGURE 17